

10045310.01000

XY:1 AP-1  
SAA1 --TAGATATG AACTCAGAGG GACTTCATTT CAGAGGCATC TGCCATGTGG<sup>391</sup>  
SAA2 TTTAGACATG AACTCACAGG GATTTCACT- CAGGGTCATC TGCCATGTGG<sup>397</sup>  
\*\*\*\*\*  
AP-2 NEIL-6/XY:1  
SAA1 CCCAGCAGAG CCCATCCTGA GGAAATGACT GGTAGAGTCA GGAGCTGGCT<sup>341</sup>  
SAA2 CCCAGCAGGG CQCATCCTGA GGAAATGACC GGTATAGTCA GGAGCTGGCT<sup>347</sup>  
\*\*\*\*\*  
YY:1  
SAA1 TCAAAGCTGC CCTCACTTCA CACCTTCCAG CAGCCCAGGT GCCGCCATCA<sup>291</sup>  
SAA2 GAAGAGCTGC CCTCACTCCA CACCTTCCAG CAGCCCAGGT GCCGCCATCA<sup>297</sup>  
\*\*\*\*\*  
NFKB AP-2 SAE  
SAA1 CGGGGCTCCC ACTCTCAACT CCGCAGCCTC AGCCCCCTCA ATGCTGAGGA<sup>241</sup>  
SAA2 CGGGGCTCCC ACTGGCATCT CTGCAGCTGC ACTTCCCCCA ATGCTGAGGA<sup>247</sup>  
\*\*\*\*\*  
-240  
SAA1 GCAGAGCTGG TCTCCTGCCC TGACAGCTGC CA-GGCACA- - - - -TC<sup>201</sup>  
SAA2 GCAGAGCTGA TCTAGACCCC TGTCCATTGC CAAGGCACAG CAAACCTCTC<sup>197</sup>  
\*\*\*\*\*  
-200 GRE NE-IL/STAT AP:1.....  
SAA1 TTGTTCCCTC AGGTTGCACA ACTGGGATAA ATGACCCGGG ATGAAGAAAC<sup>151</sup>  
SAA2 TTGTTCCCAT AGGTTACACA ACTGGGATAA ATGACCCGGG ATGAAGAAAC<sup>147</sup>  
\*\*\*\*\*  
-150 YY:1  
SAA1 CACTGGCATC CAGGAAGTTG TCTTAGACCG TTTTGTAGGG GAAATGACCT<sup>101</sup>  
SAA2 CACCGGCATC CAGGAAGTTG TCTTAGACCA GTTTGTAGGG GAAATGACCT<sup>97</sup>  
\*\*\*\*\*  
-100 NFKB  
SAA1 GCAGGGACTT TCCCAGGGA CCACATCCAG CTTTCTTCC CTCCAAGAA<sup>51</sup>  
SAA2 GCAGGGACTT TCCCAGGGA CCACATCCAG CTTTCTTCC CTCCAAGAG<sup>47</sup>  
\*\*\*\*\*  
-50 SP-1  
SAA1 ACCAGCAGGG AAGGCTCAGT ATAAATAGCA GCCACCGCTC CCTGGCAGGC<sup>1</sup>  
SAA2 ACCAGCA--- -AGGCTCACT ATAAATAGCA GCCACCTCTC CCTGGCAGAC<sup>1</sup>  
\*\*\*\*\*

FIG. 1

202210-09251001

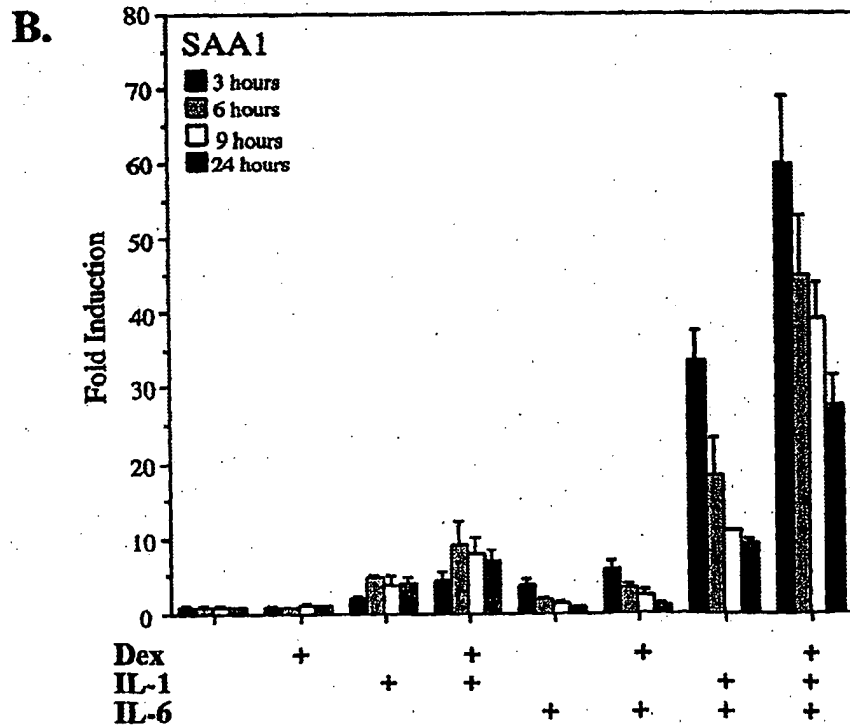
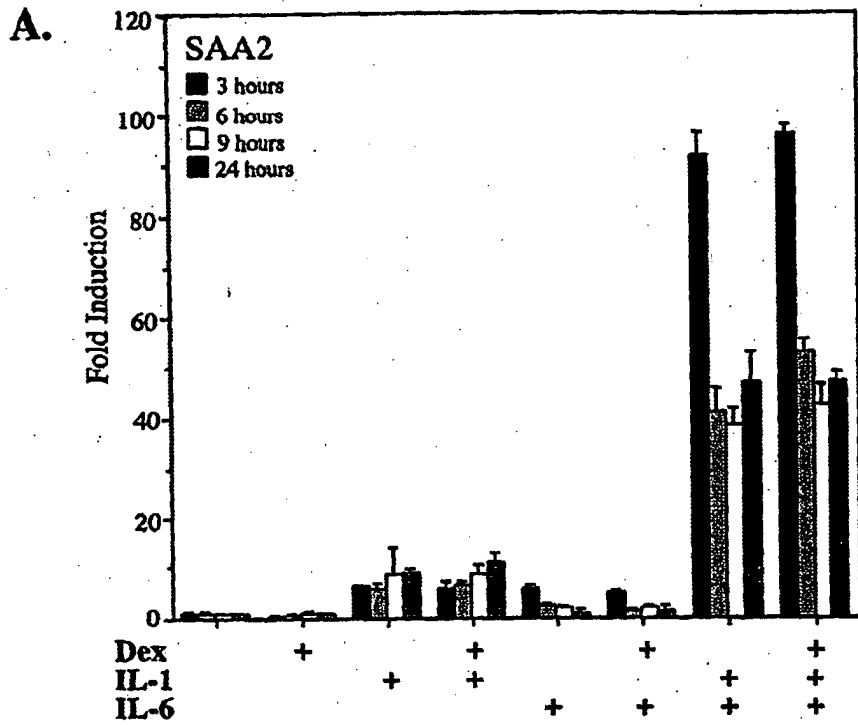


FIG. 2

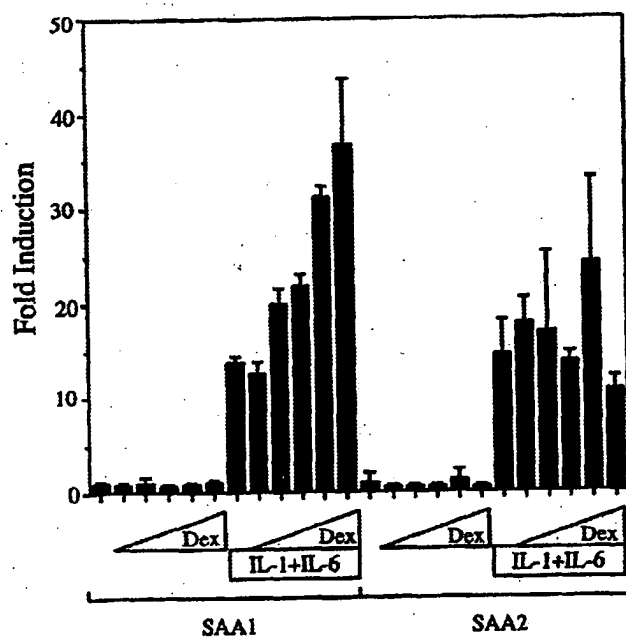


FIG. 3

2002710-0955400

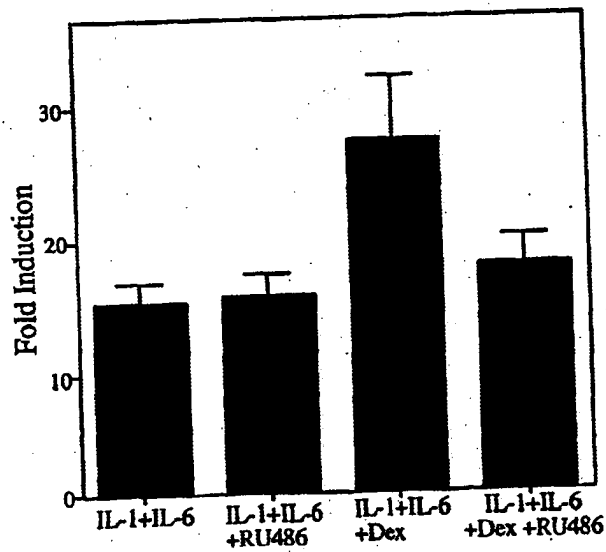


FIG. 4

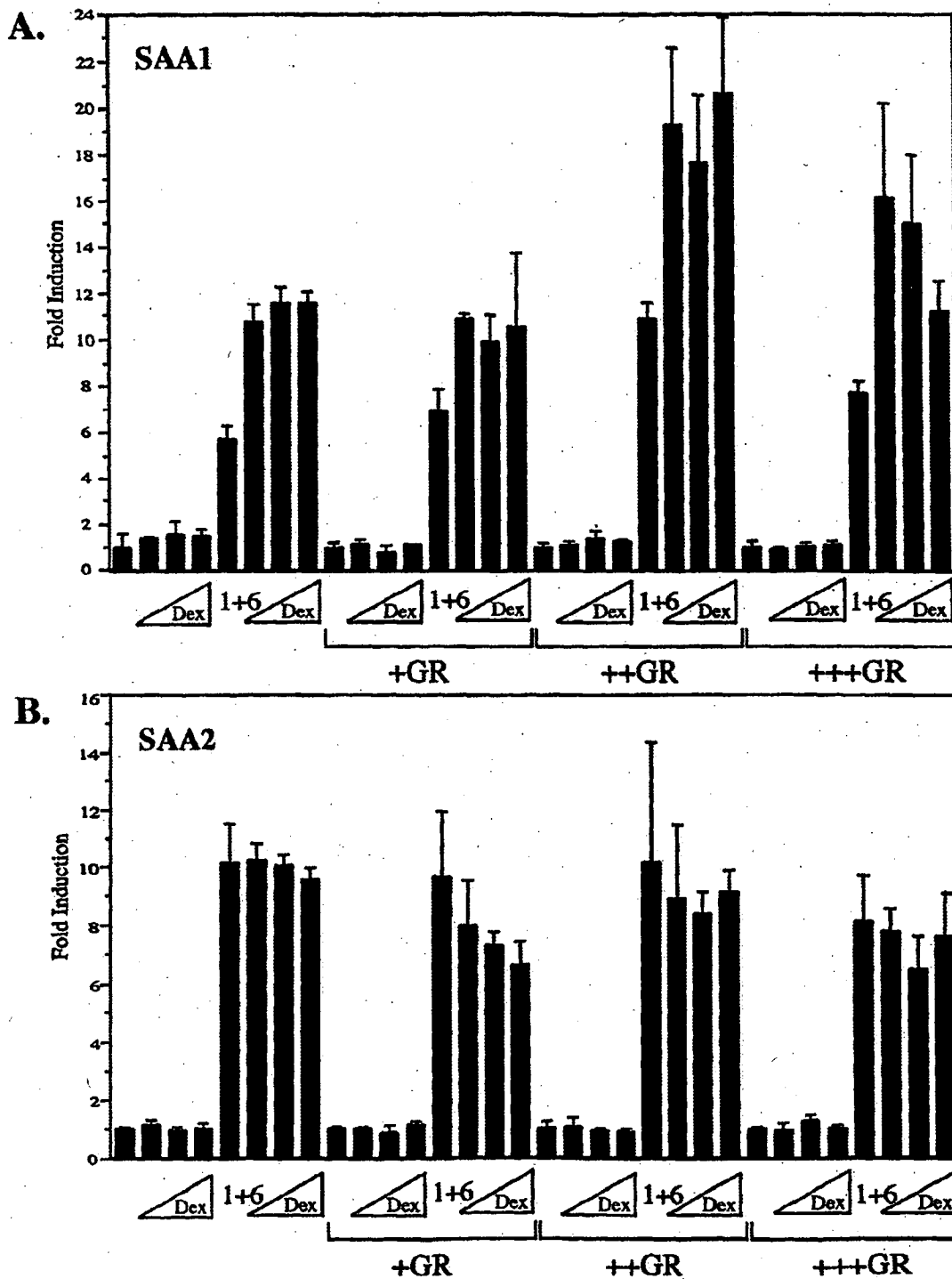


FIG. 5

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10045360.012202

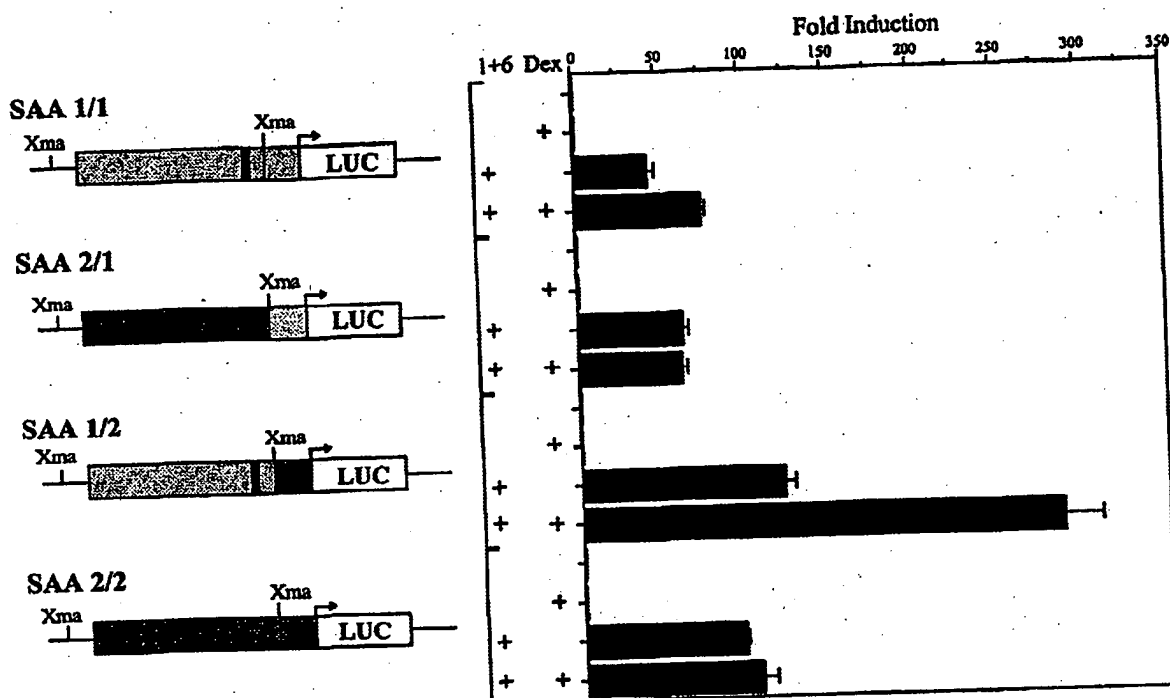


FIG. 6

A.

SAA1	CA-GGCACA-----TCTTGTTCCCTCAGGTTGCACA
GREI	CA-GGCACAGCAAACCTCTCTTGTTCCCTCAGGTTGCACA
GRE	CAAGGCACA-----TCTTGTTCCCATAGGTTACACA
SAA2	CAAGGCACAGCAAACCTCTCTTGTTCCCATAGGTTACACA
Consensus	GGTACA NNNTGTTCT
GRE	

B.

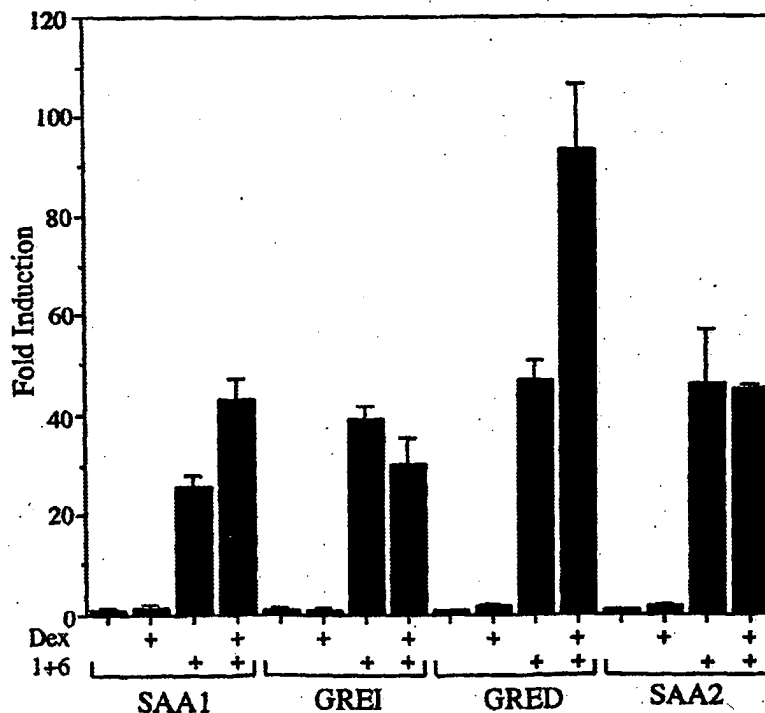


FIG. 7

202210-09254001

A.

SAA1 CAGACAAATACCTCCATGCTCGGGGGAACTATGATGCTGCCAAAAGGGGACCTGGGGGTG<sup>246</sup>  
SAA2 CAGACAAATACCTCCATGCTCGGGGGAACTATGATGCTGCCAAAAGGGGACCTGGGGGTG<sup>246</sup>

                    exon3    exon4

SAA1 TCTGGGCTGCAGAAGCGATCAG|CGATG—//—//—TGAGCTTCCTCTTCACTCTGCTC<sup>426</sup>  
SAA2 CCTGGGCCGCAGAAGTGATCAG|CAATG—//—//—TGAGCTTCCTCTTCACTCTGCTC<sup>426</sup>

SAA1 TCAGGAGATCTGGCTGTGAGGC-TCAGGGCAGGGATACAAAGC----GGGG-----<sup>472</sup>  
SAA2 TCAGGAGACCTGGCTATGAGCCCTCGGGGCAGGGATTCAAAGTTAGTGAGGTCTATGTCC<sup>486</sup>

SAA1 AGAG-----GGTACCAATGGGTATCTAATAAATACTTAAGAGGTGGAAAAA<sup>520</sup>  
SAA2 AGAGAAGCTGAGATATGGCATATAATAGGCATCTAATAAATGCTTAAGAGGTGGAAAAA<sup>546</sup>

B.

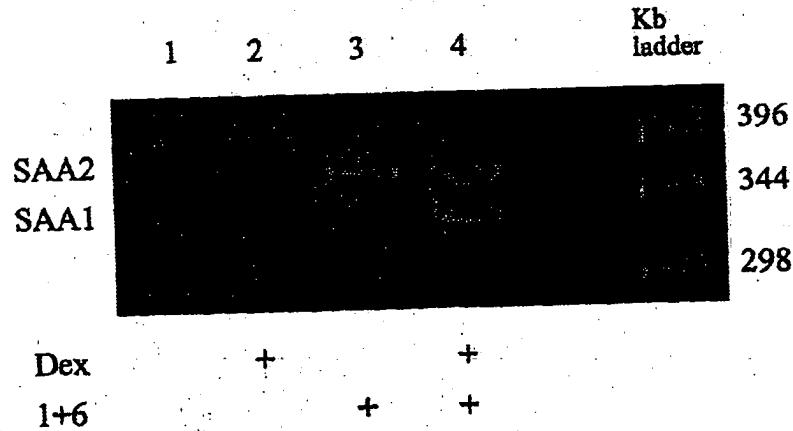


FIG. 8